**Linked Genes Clarification**

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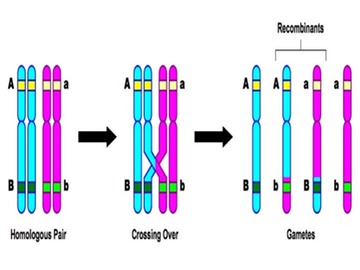
*Note: This content relates to Unit 10 (Classical Genetics), Notes Packet 3 (Chromosomal Genetics)*

**Definition of Linked Genes:**

When genes are linked, they are found on the same chromosome and are almost always inherited together, unless they are separated by crossing over (which is often called gene recombination). See image of two sets of linked alleles (A is linked to B, and “a” is linked to b) being separated by crossing over to create some “recombinants” (chromosomes with A and b, and chromosomes with “a” and B). Linked genes do not follow the rule of Independent Assortment because they are almost always inherited together. Therefore, when tracking the inheritance of unlinked genes, the offspring genotype and phenotype frequencies will NOT match the frequencies predicted by Punnett Squares. Typically the frequencies of individuals with “linked traits” are higher than the frequencies of individuals with “recombinant traits” because recombinant individuals can only be created through crossing over (see example and image below).

For example, if A codes for tall and B codes for brown hair, then tall and brown hair are linked traits (because A and B are on the same chromosome). If “a” codes for short and b codes for blond hair, then short and blond are also linked traits (because “a” and b are on the same chromosome). Therefore, tall and blond haired (A and b) individuals and short and brown haired individuals (“a” and B) can only be created through crossing over of the homologous chromosomes. Thus these “recombinant” individuals are less frequent than individuals who possess the linked gene combinations.

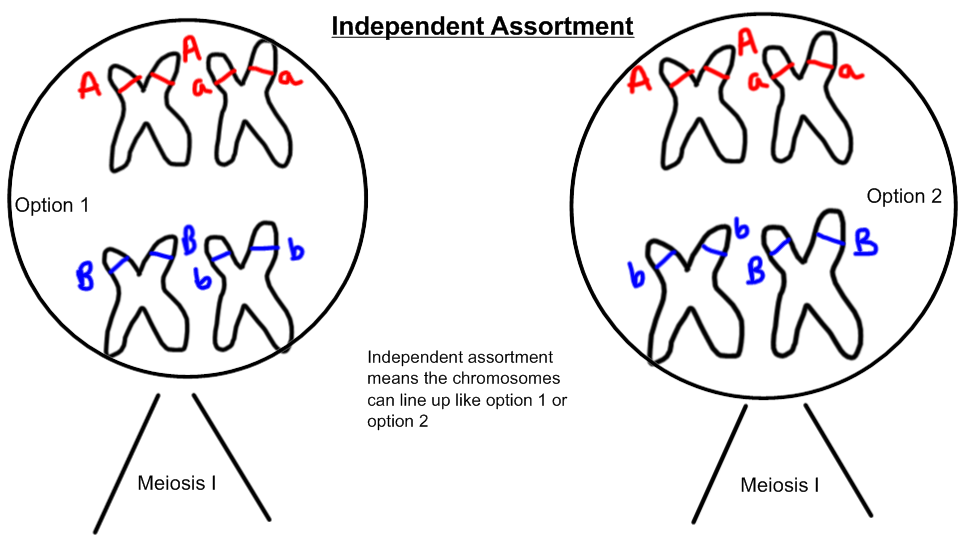
***Image #1:***

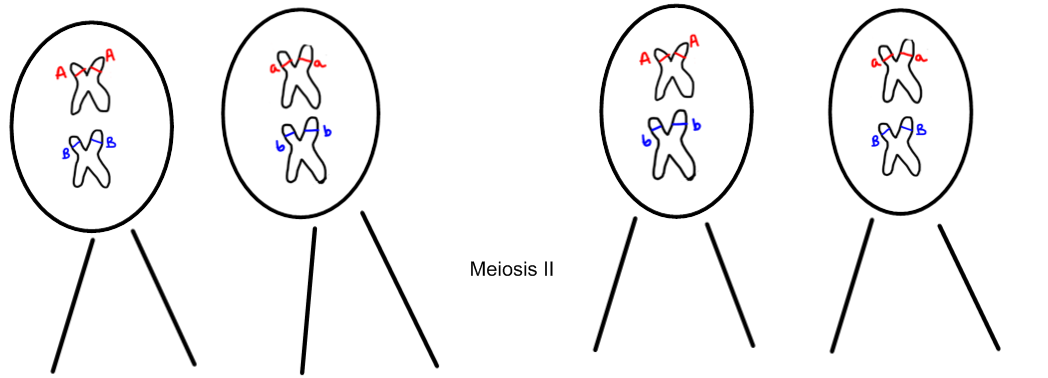


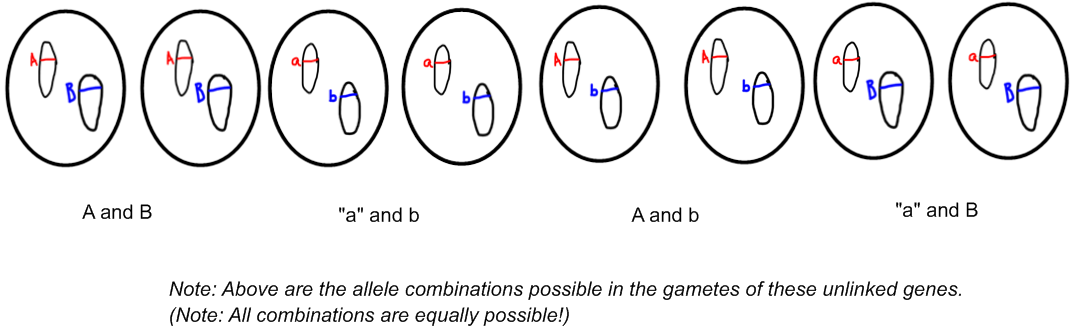
When genes are unlinked, they are found on different chromosomes. This means that they are not necessarily inherited together, and they follow the rule of independent assortment (each pair of homologous chromosomes is separated independently of the other chromosome pairs to enter the gametes). The image on the next page show independent assortment of unlinked genes A and B.

Note: As a result of independent assortment, A is just as likely to be inherited (i.e. put in the same gamete) with B as it is with b. Likewise, “a” is just as likely to be inherited with B as it is with b.

***Image #2:***







Therefore, when tracking the inheritance of unlinked genes, the offspring genotype and phenotype frequencies should match the frequencies predicted by Punnett Squares.

**Sample Genetics Problems Involving Linked vs. Unlinked Genes:**

Let’s say we are tracking the inheritance of ear length and fur color in rabbits. We will use “A” to represent the dominant long ear allele and “a” to represent the recessive short ear allele. We will use “B” to represent the dominant dark fur color allele and “b” to represent the recessive light fur color allele.

Let’s say we crossed two individuals with the genotypes AaBb and aabb. If the genes are not linked, we might see offspring phenotype frequencies like the ones given below…

***Table #1:***

|  |  |
| --- | --- |
| **Phenotypes** | **Number of Offspring** (out of 100) |
| Long Ears, Dark Fur | 23 (23%) |
| Long Ears, Light Fur | 28 (28%) |
| Short Ears, Dark Fur | 22 (22%) |
| Short Ears, Light Fur | 27 (27%) |

Note: These phenotype frequencies approximately match with the phenotype frequencies we would expect if we set up a dihybrid cross between the two parents.

***Table #2:***

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | AB | Ab | aB | ab |
| ab | AaBb | Aabb | aaBb | aabb |
| ab | AaBb | Aabb | aaBb | aabb |
| ab | AaBb | Aabb | aaBb | aabb |
| ab | AaBb | Aabb | aaBb | aabb |

I have color coded the offspring genotypes that will result in the four offspring phenotypes. A summary of the offspring phenotype ratios is given below.

Long Ears, Dark Fur (yellow) = 4/16 = 25%

Long Ears, Light Fur (green) = 4/16 = 25%

Short Ears, Dark Fur (blue) = 4/16 = 25%

Short Ears, Light Fur (pink) = 4/16 = 25%

You don’t actually need to use a dihybrid cross to solve this problem. You can use two monohybrid Punnett squares (one for the “A’s” and one for the “B’s”) and then multiply the frequencies of getting a particular ear phenotype with a particular fur phenotype to get the frequency of the two phenotypes happening together (i.e. the Multiplication Rule of Probabilities).

***Table #3:***

|  |  |  |
| --- | --- | --- |
|  | a | a |
| A | Aa | Aa |
| a | aa | aa |

***Table #4:***

|  |  |  |
| --- | --- | --- |
|  | b | b |
| B | Bb | Bb |
| b | bb | bb |

For example, the frequency of having long ears according to Table #3 is ½ and the frequency of having dark fur according to Table #4 is ½. To get the frequency of having both long ears and dark fur, you must multiply their individual probabilities.

½ x ½ = ¼ (or 25%)

If the offspring phenotype frequencies from Table #1 approximately match with the frequencies we would expect if we used Punnett squares, then the genes are unlinked (found on different chromosomes) and therefore DO follow the law of independent assortment, as shown in Image #2.

Let’s say we had different offspring phenotype frequencies for Table #1 (see below).

***Alternate Table #1***

|  |  |
| --- | --- |
| **Phenotypes** | **Number of Offspring** (out of 100) |
| Long Ears, Dark Fur | 45 (45%) |
| Long Ears, Light Fur | 6 (6%) |
| Short Ears, Dark Fur | 5 (5%) |
| Short Ears, Light Fur | 44 (44%) |

These frequencies do not match with the frequencies predicted by Punnett squares (25%, 25%, 25%, and 25%). Rather, two of the phenotypes (long ears / dark fur and short ears / light fur) are far more common than the other two phenotypes (long ears / light fur and short ears / dark fur). Therefore, the alleles for long ears and dark fur (A and B) are linked (found on the same chromosome). The alleles for short ears and light fur (“a” and b) are also linked. The other two possible phenotypes—long ears / light fur (A and b) and short ears / dark fur (“a” and B) are only created through crossing over, as shown in Image #1.

What if the parent genotypes are not AaBb x aabb? Let’s say our parent genotypes are AaBb and AaBb. If we completed a Punnett square analysis for these parent genotypes, we would have the following phenotype frequencies in our offspring: 9/16 (56%) long ears / dark fur, 3/16 (19%) long ears / light fur, 3/16 (19%) short ears / dark fur, and 1/16 (6%) short ears / light fur. If our frequencies from an actual experimental breeding are similar to the ones given below in Table #5, then the genes are unlinked, since they appear to match the frequencies predicted by Punnett squares.

If the genes are linked (A to B and “a” to b), we would expect to see frequencies like those given in Alternate Table #1, where two phenotypes (long ears / dark fur and short ears / light fur) are far more common than the other two phenotypes (long ears / light fur and short ears / dark fur).

***Table #5:***

|  |  |
| --- | --- |
| **Phenotypes** | **Number of Offspring** (out of 100) |
| Long Ears, Dark Fur | 58 (58%) |
| Long Ears, Light Fur | 18 (18%) |
| Short Ears, Dark Fur | 17 (17%) |
| Short Ears, Light Fur | 7 (7%) |